

## SEQUENCE LISTING

&lt;110&gt; EXELIXIS, INC.

&lt;120&gt; PSMCS AS MODIFIERS OF THE RB PATHWAY AND METHODS OF USE

&lt;130&gt; EX03-059C-PC

&lt;150&gt; US 60/401,737

&lt;151&gt; 2002-08-07

&lt;150&gt; US 60/428,872

&lt;151&gt; 2002-11-25

&lt;160&gt; 11

&lt;170&gt; PatentIn version 3.2

&lt;210&gt; 1

&lt;211&gt; 1478

&lt;212&gt; DNA

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 <212> PRT  
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<400> 10

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 1 5 10 15

Lys Asp Asp Lys Pro Ile Arg Ala Leu Asp Glu Gly Asp Ile Ala Leu  
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Leu Lys Thr Tyr Gly Gln Ser Thr Tyr Ser Arg Gln Ile Lys Gln Val  
 35 40 45  
 Glu Asp Asp Ile Gln Gln Leu Leu Lys Lys Ile Asn Glu Leu Thr Gly  
 50 55 60  
 Ile Lys Glu Ser Asp Thr Gly Leu Ala Pro Pro Ala Leu Trp Asp Leu  
 65 70 75 80  
 Ala Ala Asp Lys Gln Thr Leu Gln Ser Glu Gln Pro Leu Gln Val Ala  
 85 90 95  
 Arg Cys Thr Lys Ile Ile Asn Ala Asp Ser Glu Asp Pro Lys Tyr Ile  
 100 105 110  
 Ile Asn Val Lys Gln Phe Ala Lys Phe Val Val Asp Leu Ser Asp Gln  
 115 120 125  
 Val Ala Pro Thr Asp Ile Glu Glu Gly Met Arg Val Gly Val Asp Arg  
 130 135 140  
 Asn Lys Tyr Gln Ile His Ile Pro Leu Pro Pro Lys Ile Asp Pro Thr  
 145 150 155 160  
 Val Thr Met Met Gln Val Glu Glu Lys Pro Asp Val Thr Tyr Ser Asp  
 165 170 175  
 Val Gly Gly Cys Lys Glu Gln Ile Glu Lys Leu Arg Glu Val Val Glu  
 180 185 190  
 Thr Pro Leu Leu His Pro Glu Arg Phe Val Asn Leu Gly Ile Glu Pro  
 195 200 205  
 Pro Lys Gly Val Leu Leu Phe Gly Pro Pro Gly Thr Gly Lys Thr Leu  
 210 215 220  
 Cys Ala Arg Ala Val Ala Asn Arg Thr Asp Ala Cys Phe Ile Arg Val  
 225 230 235 240  
 Ile Gly Ser Glu Leu Val Gln Lys Tyr Val Gly Glu Gly Ala Arg Met  
 245 250 255  
 Val Arg Glu Leu Phe Glu Met Ala Arg Thr Lys Lys Ala Cys Leu Ile  
 260 265 270

Phe Phe Asp Glu Ile Asp Ala Ile Gly Gly Ala Arg Phe Asp Asp Gly  
 275 280 285

Ala Gly Gly Asp Asn Glu Val Gln Arg Thr Met Leu Glu Leu Ile Asn  
 290 295 300

Gln Leu Asp Gly Phe Asp Pro Arg Gly Asn Ile Lys Val Leu Met Ala  
 305 310 315 320

Thr Asn Arg Pro Asp Thr Leu Asp Pro Ala Leu Met Arg Pro Gly Arg  
 325 330 335

Leu Asp Arg Lys Ile Glu Phe Ser Leu Pro Asp Leu Glu Gly Arg Thr  
 340 345 350

His Ile Phe Lys Ile His Ala Arg Ser Met Ser Val Glu Arg Asp Ile  
 355 360 365

Arg Phe Glu Leu Leu Ala Arg Leu Cys Pro Asn Ser Thr Gly Ala Glu  
 370 375 380

Ile Arg Ser Val Cys Thr Glu Ala Gly Met Phe Ala Ile Arg Ala Arg  
 385 390 395 400

Arg Lys Ile Ala Thr Glu Lys Asp Phe Leu Glu Ala Val Asn Lys Val  
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Ile Lys Ser Tyr Ala Lys Phe Ser Ala Thr Pro Arg Tyr Met Thr Tyr  
 420 425 430

Asn

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 <212> PRT  
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<400> 11

Met Pro Asp Tyr Leu Gly Ala Asp Gln Arg Lys Thr Lys Glu Asp Glu  
 1 5 10 15

Lys Asp Asp Lys Pro Ile Arg Ala Leu Asp Glu Gly Asp Ile Ala Leu  
 20 25 30

Leu Lys Thr Tyr Gly Gln Ser Thr Tyr Ser Arg Gln Ile Lys Gln Val  
 35 40 45

Glu Asp Asp Ile Gln Gln Leu Leu Lys Lys Ile Asn Glu Leu Thr Gly  
 50 55 60

Ile Lys Glu Ser Asp Thr Gly Leu Ala Pro Pro Ala Leu Trp Asp Leu  
 65 70 75 80

Ala Ala Asp Lys Gln Thr Leu Gln Ser Glu Gln Pro Leu Gln Val Ala  
 85 90 95

Arg Cys Thr Lys Ile Ile Asn Ala Asp Ser Glu Asp Pro Lys Tyr Ile  
 100 105 110

Ile Asn Val Lys Gln Phe Ala Lys Phe Val Val Asp Leu Ser Asp Gln  
 115 120 125

Val Ala Pro Thr Asp Ile Glu Glu Gly Met Arg Val Gly Val Asp Arg  
 130 135 140

Asn Lys Tyr Gln Ile His Ile Pro Leu Pro Pro Lys Ile Asp Pro Thr  
 145 150 155 160

Val Thr Met Met Gln Val Glu Glu Lys Pro Asp Val Thr Tyr Ser Asp  
 165 170 175

Val Gly Gly Cys Lys Glu Gln Ile Glu Lys Leu Arg Glu Val Val Glu  
 180 185 190

Thr Pro Leu Leu His Pro Glu Arg Phe Val Asn Leu Gly Ile Glu Pro  
 195 200 205

Pro Lys Gly Val Leu Leu Phe Gly Pro Pro Gly Thr Gly Lys Thr Leu  
 210 215 220

Cys Ala Arg Ala Val Ala Asn Arg Thr Asp Ala Cys Phe Ile Arg Val  
 225 230 235 240

Ile Gly Ser Glu Leu Val Gln Lys Tyr Val Gly Glu Gly Ala Arg Met  
 245 250 255

Val Arg Glu Leu Phe Glu Met Ala Arg Thr Lys Lys Ala Cys Leu Ile  
 260 265 270

Phe Phe Asp Glu Ile Asp Ala Ile Gly Gly Ala Arg Phe Asp Asp Gly  
 275 280 285

Ala Gly Gly Asp Asn Glu Val Gln Arg Thr Met Leu Glu Leu Ile Asn

290	295	300															
Gln	Leu	Asp	Gly	Phe	Asp	Pro	Arg	Gly	Asn	Ile	Lys	Val	Leu	Met	Ala		
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Thr	Asn	Arg	Pro	Asp	Thr	Leu	Asp	Pro	Ala	Leu	Met	Arg	Pro	Gly	Arg		
				325					330					335			
Leu	Asp	Arg	Lys	Ile	Glu	Phe	Ser	Leu	Pro	Asp	Leu	Glu	Gly	Arg	Thr		
			340					345					350				
His	Ile	Phe	Lys	Ile	His	Ala	Arg	Ser	Met	Ser	Val	Glu	Arg	Asp	Ile		
		355					360					365					
Arg	Phe	Glu	Leu	Leu	Ala	Arg	Leu	Cys	Pro	Asn	Ser	Thr	Gly	Ala	Glu		
	370					375					380						
Ile	Arg	Ser	Val	Cys	Thr	Glu	Ala	Gly	Met	Phe	Ala	Ile	Arg	Ala	Arg		
385					390					395					400		
Arg	Lys	Ile	Ala	Thr	Glu	Lys	Asp	Phe	Leu	Glu	Ala	Val	Asn	Lys	Val		
				405					410					415			
Ile	Lys	Ser	Tyr	Ala	Lys	Phe	Ser	Ala	Thr	Pro	Arg	Tyr	Met	Thr	Tyr		
			420					425					430				

Asn